SPECIFICATION

NOVEL POLYPEPTIDE HAVING WATER CHANNEL ACTIVITY AND DNA SEQUENCE

TECHNICAL FIELD

The present invention relates to a novel, human adipose tissue-derived polypeptide having water channel activity and to a DNA sequence encoding for the polypeptide.

BACKGROUND ART

The permeation of water through a cell membrane generally occurs slowly by way of diffusion into the lipid bilayer which is the main structure of the cell membrane. Recently, however, it was discovered that, in certain kinds of cells, water is transferred rapidly through the cell membrane, suggesting the involvement in the above phenomenon of some membrane protein selectively permeable to water. Thereafter, such membrane proteins of various kinds have actually been isolated. Such membrane proteins are designated as water channels. In this specification, the function of the above water channels which has selective permeation of water through the cell membrane is referred to as "water channel activity". The water channels may be permeable to water alone or permeable to not only water but also low-molecular-weight substances such as glycerol and urea.

As a membrane protein having such water channel activity, there have been isolated a group of membrane proteins known as aquapolins (AQPs). Furthermore, some aquapolin genes have so far been cloned, and aquapolins such as AQP1 through AQP5, FA-CHIP and AQP-γTIP have been discovered in mammals, amphibians, plants, etc. [cf. e.g. Akira Sasaki, Igaku no Ayumi (Advances in Medicine), vol. 173, No. 9, 1995].

P. Agre et al. reported, in Science (vol. 256, pp. 385 to 387, 1992) that Xenopus laevis oocytes in which the in vitro

transcript RNA for CHIP28, the current designation of which is AQP1, had been introduced showed increased water permeability. In Science (vol. 264, pp. 92 to 95, 1994), B. A. van Oost et al. disclosed the amino acid sequence of human AQP2 and suggested that this should be involved in vasopressin-dependent urine concentration.

In Proc. Natl. Acad. Sci. USA (vol. 91, pp. 6269 to 6273, 1994), Ishibashi et al. disclosed the nucleotide sequence of the gene for renal collecting tubule-derived AQP3 and the amino acid sequence encoded thereof. Ishibashi et al. confirmed its water channel activity by injecting the AQP3 cRNA into Xenopus laevis oocytes and measuring the water permeability thereof. Ishibashi et al. reported that this AQP3 transported not only water but also nonionic small molecules such as urea and glycerol.

In Proc. Natl. Acad. Sci. USA (vol. 91, pp. 13052 to 13056, 1994), J. S. Jung et al. reported about the isolation of AQP4. This AQP4 is known to occur most abundantly in mammalian brains and have mercury resistance. In J. Biol. Chem. (vol. 270, pp. 1908 to 1912, 1995), S. Raina et al. who prepared rat salivary gland-derived AQP5 cDNA describe the nucleotide sequence of the cDNA and the amino acid sequence encoded thereby. S. Raina et al. cloned the cDNA by utilizing the occurrence of an NPA sequence and confirmed its function by observing that the cRNA enhances the water permeability of Xenopus laevis oocytes.

The aquapolin family mentioned above is considered to be involved in water metabolism in mammals and, for example, it has been confirmed that AQP2 is found only in the renal collecting tubule luminal membrane, which is indicative of its close association with the vasopressin-urea concentration system, and its involvement in renal diseases has become acknowledged. Therefore, such membrane proteins having water channel activity are of importance in any attempt to develop novel therapies for water-associated diseases.

Meanwhile, the expression of the aqupolin family

mentioned above has been confirmed in such organs as kidney, brain, gall bladder, eye, intestine, salivary gland and bronchus but there is no report as yet about the occurrence of membrane proteins having water channel activity in other organs or tissues, particularly in adipose tissue.

SUMMARY OF THE INVENTION

In view of the above-mentioned state of the art, the present invention has for its object to provide a novel membrane protein having water channel activity and a DNA sequence encoding for the polypeptide.

The present invention is related to a novel polypeptide having water channel activity which has the amino acid sequence, within the molecule thereof, shown in the sequence listing under SEQ ID NO:1.

The present invention is also related to a nucleotide sequence itself which codes for a polypeptide having, within the molecule thereof, the amino acid sequence shown in the sequence listing under SEQ ID NO:1 and having water channel activity.

The present invention is further related to the DNA sequence shown in the sequence listing under SEQ ID NO:2.

The present invention is still further related to a polypeptide having water channel activity which has the amino acid sequence, within the molecule thereof, encoded by the nucleotide No. 173 to No. 1198 of the nucleotide sequence shown in the sequence listing under SEQ ID NO:2.

DETAILED DESCRIPTION OF THE INVENTION

In the following, the present invention is described in detail.

The polypeptide of the present invention has the amino acid sequence shown in the sequence listing under SEQ ID NO:1. This polypeptide has a sequence composed of three amino acids, namely asparagine-proline-alanine, as the amino acid Nos. 195

to 197. However, the characteristic feature common to the so-far known AQPs, that said asparagine-proline-alanine sequence occurs twice, is not found in the polypeptide of the present invention. That this polypeptide has water channel activity can be confirmed from the fact that it enhances the water permeability of Xenopus laevis oocytes.

The above polypeptide may be generated by translation by a protein synthesis system constituted, in vivo or in vitro, based on the nucleotide sequence coding for the amino acid sequence of said polypeptide. The nucleotide sequence of the present invention substantially has a region coding for the amino acid sequence of said polypeptide and, where necessary, may contain one or more other regions such as a promoter region. In the protein synthesis based on genetic information, the information carried by the gene DNA is transcribed into mRNA as the result of DNA-dependent RNA synthesis aided by RNA polymerase. And, this mRNA is translated into the amino acid sequence in a tRNA-containing protein synthesis system. Therefore, the nucleotide sequence of the present invention includes not only the DNA sequence but also the RNA sequence. Furthermore, since it is generally known that, for an amino acid, there is one or a plurality of codons corresponding thereto, it is a matter of course that the above-mentioned nucleotide sequence is not limited to only one sequence but may include nucleotide sequences resulting from substitution of another synomyous codon coding for the same amino acid.

The above polypeptide can be formed based on the genetic information carried by the DNA sequence shown in the sequence listing under SEQ ID NO:2. This polypeptide is encoded by that portion of the nucleotide sequence shown in the sequence listing under SEQ ID NO:2 which ranges from the nucleotide No. 173 to No. 1198. Of the DNA sequence shown in the sequence listing under SEQ ID NO:2, the nucleotide sequences other than the portion of said nucleotide numbers are noncoding regions, among which the polyadenylation consensus sequence AATAAA occurs at

the nucleotide No.1234 to No.1239. Other possible reading frames of said DNA sequence shown under SEQ ID NO:2 can be excluded from consideration, since the polypeptides encoded are very small-sized, hence considered to be incapable of performing any water channel function.

It has been confirmed by the inventors that the full-length sequence of the above nucleic acid bases has no counterpart sequence either in GenBank or in dbEST.

The polypeptide of the present invention has water channel activity in adipose tissue. While adipose tissue is distributed in various parts of the living organism, the polypeptide of the present invention has an action to control the transfer of water in such adipose tissue and is expected to be effective in upholding normal functions of adipose tissue at various sites.

BEST MODES FOR CARRYING OUT THE INVENTION

The above-mentioned DNA sequence given under SEQ ID NO:2 corresponds to the nucleotide sequence of cDNA obtained from human adipose tissue by cloning. Human adipose tissue is a tissue which stores fat as energy reserves. It is known that various proteins are formed in this adipose tissue. A 3'-directed DNA library is known as a cDNA library from which the genes actually expressed in this adipose tissue or, in other words, the mRNA composition in this adipose tissue can be copied faithfully. This 3'-directed DNA library contains only those specified 3'-terminal regions of mRNAs which range from poly(A) to the MboI site which is a restriction enzyme recognition site upstream of said poly(A) and, therefore, said library is suited for template preparation by the PCR technique. Therefore, by extracting a clone from this library and using it to determine a longer nucleotide sequence including the amino acid coding region from this complete adipose tissue cDNA library, it becomes possible to obtain the genetic information concerning the protein which is actually formed in adipose tissue. The

DNA sequence of the present invention as shown under the above-mentioned SEQ ID NO:2 is found by such cloning. A method of obtaining the cDNA by cloning from human adopose tissue is now described in detail.

Known as said method is, for example, the method described in Biochem. Biophys. Res. Commun., 221, 286 to 289 (1996). According to this method, the total RNA is first separated from adipose tissue and, when necessary, purified to give poly(A) RNA. For this purification, commercially available purification kits can be used. For example, Pharmacia's Quick prep mRNA purification kit or the like in which oligo(dT)-cellulose and various buffers are used in combination can judiciously be employed. Then, a double-stranded cDNA is synthesized using a pUC19 system vector primer and the double-stranded cDNA so synthesized is selectively cleaved with the restriction enzyme MboI (which recognizes the nucleotide sequence GATC). On that occasion, the GATC sequence on the vector molecule side, which can be methylated to give $G^{m}ATC$ when replication is effected in dam^{+} bacterial cells, is not cleaved with MboI. As the cleaved cDNA is subjected to self-cyclization using E. coli ligase, a plasmid containing a cDNA fragment extending from poly(A) to the nearest MboI site is completed. This plasmid is introduced into Escherichia coli, followed by cultivation and selection of a transformant E. coli colony. Then, the cDNA in said colony is amplified by the PCR technique using appropriate PCR primers.

On the other hand, the full-length double-stranded cDNA synthesized using the pUC19 system vector primer is cleaved at the 5' end using T4 polymerase and subjected to cyclization using T4 ligase and introduction into Escherichia coli for transformation. From among the thus-obtained transformant colonies, the desired colony is obtained by screening using, as a probe, a labeled form of the adipose tissue-specific cDNA obtained from said 3'-directed DNA library by the method mentioned above. The insert cDNA in this colony is amplified

by the PCR technique using appropriate PCR primers. The amplification product is purified and, after sonication, subcloned into the M13 phage.

The nucleotide sequence of the thus-cloned cDNA can be determined, for example, by reaction with a primer dye, purification and analysis using an automated sequencer or the like. In this manner, the DNA sequence of the present invention can be obtained.

The polypeptide of the present invention has water channel activity. This water channel activity can be confirmed by observing an enhancement of water permeability in Xenopus laevis oocytes. It is known that no AQP family gene has been expressed in Xenopus laevis oocytes and, therefore, any increase in water permeability as caused by the injected mRNA can be easily confirmed. For this reason, said oocytes are widely used in confirming water channel activity. For example, in Proc. Natl. Acad. Sci. USA, vol. 91, pp. 6269 to 6273 (1994), Ishibashi et al. confirmed the water channel activity by inserting the AQP3 cDNA into the pSP64T-derived BlueScript vector, synthesizing the cRNA using T7 RNA polymerase, injecting this cRNA into Xenopus laevis oocytes and, after 48 to 62 hours of incubation following injection, observing an increase in water permeability and in the volume of the oocyte.

The polypeptide encoded by the DNA sequence of the present invention can be identified by analyzing the amino acid sequence of the polypeptide synthesized in an Escherichia coli protein synthesis system constituted in vitro. In this case, the methods of identifying N-and C-terminal sequences of expression products as described in Shin Seikagaku Jikken Koza (Experiments in Biochemistry, A New Course) 1 (published by Tokyo Kagaku Dojin), pages 22 to 24 can be employed.

The following examples illustrate the present invention in further detail. These examples are, however, by no means limitative of the scope of the present invention.

Example 1

Determination of DNA nucleotide sequence

According to a recent report [Biochem. Biophys. Res. Commun., 221, 286 to 289 (1996)], a DNA for an adipose tissue-specific collagen-like factor has been cloned using a 3'-directed DNA library containing only those specified 3'-terminal regions of RNA molecules which range from poly(A) to the restriction enzyme MboI site upstream thereof [Nature Genet., 2, 173 to 179 (1992)], which library makes it possible not only to identify the gene under expression but also to examine the frequency of expression or amount of expression. In accordance with the method described in the above report, the DNA nucleotide sequence of the present invention was determined using an adipose tissue-specific 3'-directed DNA library.

Method

Reverse transcriptase was added to poly(A)$^+$ RNA separated and purified from human adipose tissue using a Quick prep mRNA purification kit, followed by insertion into λ ZAP II containing the pUC19 system vector pBluescript and introduction into Escherichia coli. Screening carried out using an adipose tissue-specific partial DNA as a probe gave a colony of transformant Escherichia coli. Then, together with two primers (SK: 5'CGCTCTAGAACTAGTGGATC3'; T7: 5'GTAATACGACTCACTATAGGGC3'), PCR [polymerase chain reaction; (30 seconds at 95℃ + 30 seconds at 50℃ + 60 seconds at 70℃) x 15 cycles, followed by (30 seconds at 95℃ + 60 seconds at 70℃) x 15 cycles], was carried out and, after sonication, the product was subcloned in M13. A primer dye was added thereto and, after purification, the nucleotide sequence of the DNA was analyzed using an automated sequencer. The nucleotide sequence obtained is shown in the sequence listing under SEQ ID NO:2.

Example 2

Examination as to water permeability

As for the studies on the water permeability of the AQP family, there are reports about AQP1 [Science, 256, 385-387 (1992)] and AQP3 [Proc. Natl. Acad. Sci. USA, 91, 6269-6273 (1994)] in which RNA was introduced into Xenopus laevis oocytes, in which AQP family genes have not been expressed, and then the water permeability was calculated from changes in the surface area and volume of said oocytes in a hypotonic culture medium. Therefore, the membrane protein encoded by the DNA of the present invention was checked for water permeability according to the method described in the references cited above.

Test method

The RNA (10 ng) obtained in Example 1 from human adipose tissue was introduced into Xenopus laevis oocytes by microinjection and the oocytes were incubated at 20℃ for 3 days in an isotonic culture medium (about 200 mOsm). The cultured oocytes were transferred to a hypotonic culture medium (about 40 mOsm). Photograph was taken 20 seconds and 40 seconds after transfer, and the sectional area and volume of each oocyte were determined using an image analyzer. The water permeability of the membrane protein was calculated as follows:

$$\text{Permeability (cm/sec)} = [(V_{40}-V_{20})/20]/[(A_{20}\times 10^{-2}\times 4)\times 1.384]$$

where V_{20} denotes the oocyte volume (cm^3) after 20 seconds, V_{40} denotes the oocyte volume (cm^3) after 40 seconds, and A_{20} denotes the oocyte sectional area (mm^2) after 20 seconds.

The result is shown in Table 1. The water permeability found when purified water was used for microinjection in lieu of the RNA is also shown.

Further, the expression of the polypeptide of the present

invention in said oocytes was confirmed by a C-terminal region immunoassay using the rabbit antiserum obtained by using the polypeptide of the present invention as synthesized in vitro.

Table 1

	Water permeability (cm/sec)
Group in which RNA introduction was not made	30.0×10^{-4}
Group in which RNA introduction was made	292.5×10^{-4}

As is evident from Table 1, the polypeptide encoded by the DNA sequence of the present invention caused an increase in water permeability after introduction into the oocytes. This result indicate that the polypeptide of the present invention has water channel activity.

INDUSTRIAL UTILIZABILITY

The present invention provides a novel protein having water channel activity and a novel DNA sequence encoding the protein. Said protein is one found in human adipose tissue for which the occurrence of water channels has not been reported as yet. The present invention makes it possible to develop novel therapies for water or fat metabolism-associated diseases in which said tissue is involved.

[Sequence listings]

SEQ ID No.: 1
Length: 342
Type: amino acid
Topology: linear
Species: peptide

Sequence

Met	Val	Gln	Ala	Ser	Gly	His	Arg	Arg	Ser	Thr	Arg	Gly	Ser	Lys	Met
				5					10					15	
Val	Ser	Trp	Ser	Val	Ile	Ala	Lys	Ile	Gln	Glu	Ile	Leu	Gln	Arg	Lys
			20					25					30		
Met	Val	Arg	Glu	Phe	Leu	Ala	Glu	Phe	Met	Ser	Thr	Tyr	Val	Met	Met
		35					40					45			
Val	Phe	Gly	Leu	Gly	Ser	Val	Ala	His	Met	Val	Leu	Asn	Lys	Lys	Tyr
	50					55					60				
Gly	Ser	Tyr	Leu	Gly	Val	Asn	Leu	Gly	Phe	Gly	Phe	Gly	Val	Thr	Met
65					70					75					80
Gly	Val	His	Val	Ala	Gly	Arg	Ile	Ser	Gly	Ala	His	Met	Asn	Ala	Ala
				85					90					95	
Val	Thr	Phe	Ala	Asn	Cys	Ala	Leu	Gly	Arg	Val	Pro	Trp	Arg	Lys	Phe
			100					105					110		
Pro	Val	Tyr	Val	Leu	Gly	Gln	Phe	Leu	Gly	Ser	Phe	Leu	Ala	Ala	Ala
		115					120					125			
Thr	Ile	Tyr	Ser	Leu	Phe	Tyr	Thr	Ala	Ile	Leu	His	Phe	Ser	Gly	Gly
	130					135					140				
Gln	Leu	Met	Val	Thr	Gly	Pro	Val	Ala	Thr	Ala	Gly	Ile	Phe	Ala	Thr
145					150					155					160
Tyr	Leu	Pro	Asp	His	Met	Thr	Leu	Trp	Arg	Gly	Phe	Leu	Asn	Glu	Ala
				165					170					175	
Trp	Leu	Thr	Gly	Met	Leu	Gln	Leu	Cys	Leu	Phe	Ala	Thr	Thr	Asp	Gln
			180					185					190		
Glu	Asn	Asn	Pro	Ala	Leu	Pro	Gly	Thr	Glu	Ala	Leu	Val	Ile	Gly	Ile
		195					200					205			

Leu Val Val Ile Ile Gly Val Ser Leu Gly Met Asn Thr Gly Tyr Ala
210 215 220
Ile Asn Pro Ser Arg Asp Leu Pro Pro Arg Ile Phe Thr Phe Ile Ala
225 230 235 240
Gly Trp Gly Lys Gln Val Phe Ser Asn Gly Glu Asn Trp Trp Trp Val
245 250 255
Pro Val Val Ala Pro Leu Leu Gly Ala Tyr Leu Gly Gly Ile Ile Tyr
260 265 270
Leu Val Phe Ile Gly Ser Thr Ile Pro Arg Glu Pro Leu Lys Leu Glu
275 280 285
Asp Ser Val Ala Tyr Glu Asp His Gly Ile Thr Val Leu Pro Lys Met
290 295 300
Gly Ser His Glu Pro Thr Ile Ser Pro Leu Thr Pro Val Ser Val Ser
305 310 315 320
Pro Ala Asn Arg Ser Ser Val His Pro Ala Pro Pro Leu His Glu Ser
325 330 335
Met Ala Leu Glu His Phe
340

SEQ ID No: 2
Length: 1258
Type: nucleotide
Strandedness: double strand
Topology: linear
Species: cDNA to mRNA
Original source
Organism: human
Tissue type: adipose tissue
Feature Information
Name/Key: peptide
Location: 173..1198
Identification method: E

Sequence

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GGCTCTGGAC TGGGGACACA GGGATAGCTG AGCCCCAGCT GGGGGTGGAA GCTGAGCCAG   60
GGACAGTCAC GGAGGAACAA GATCAAGATG CGCTGTAACT GAGAAGCCCC CAAGGCGGAG  120
GCTGAGAATC AGAGACATTT CAGCAGACAT CTACAAATCT GAAAGACAAA AC ATG GTT  178
                                                          Met Val
                                                            1
CAA GCA TCC GGG CAC AGG CGG TCC ACC CGT GGC TCC AAA ATG GTC TCC     226
Gln Ala Ser Gly His Arg Arg Ser Thr Arg Gly Ser Lys Met Val Ser
          5                  10                  15
TGG TCC GTG ATA GCA AAG ATC CAG GAA ATA CTG CAG AGG AAG ATG GTG     274
Trp Ser Val Ile Ala Lys Ile Gln Glu Ile Leu Gln Arg Lys Met Val
     20                  25                  30
CGA GAG TTC CTG GCC GAG TTC ATG AGC ACA TAT GTC ATG ATG GTA TTC     322
Arg Glu Phe Leu Ala Glu Phe Met Ser Thr Tyr Val Met Met Val Phe
 35                  40                  45                  50
GGC CTT GGT TCC GTG GCC CAT ATG GTT CTA AAT AAA AAA TAT GGG AGC     370
Gly Leu Gly Ser Val Ala His Met Val Leu Asn Lys Lys Tyr Gly Ser
                 55                  60                  65
TAC CTT GGT GTC AAC TTG GGT TTT GGC TTC GGA GTC ACC ATG GGA GTG     418
Tyr Leu Gly Val Asn Leu Gly Phe Gly Phe Gly Val Thr Met Gly Val
             70                  75                  80
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CAC GTG GCA GGC CGC ATC TCT GGA GCC CAC ATG AAC GCA GCT GTG ACC     466
His Val Ala Gly Arg Ile Ser Gly Ala His Met Asn Ala Ala Val Thr
          85                  90                  95
TTT GCT AAC TGT GCG CTG GGC CGC GTG CCC TGG AGG AAG TTT CCG GTC     514
Phe Ala Asn Cys Ala Leu Gly Arg Val Pro Trp Arg Lys Phe Pro Val
     100                 105                 110
TAT GTG CTG GGG CAG TTC CTG GGC TCC TTC CTG GCG GCT GCC ACC ATC     562
Tyr Val Leu Gly Gln Phe Leu Gly Ser Phe Leu Ala Ala Ala Thr Ile
115                 120                 125                 130
TAC AGT CTC TTC TAC ACG GCC ATT CTC CAC TTT TCG GGT GGA CAG CTG     610
Tyr Ser Leu Phe Tyr Thr Ala Ile Leu His Phe Ser Gly Gly Gln Leu
                135                 140                 145
ATG GTG ACC GGT CCC GTC GCT ACA GCT GGC ATT TTT GCC ACC TAC CTT     658
Met Val Thr Gly Pro Val Ala Thr Ala Gly Ile Phe Ala Thr Tyr Leu
          150                 155                 160
CCT GAT CAC ATG ACA TTG TGG CGG GGC TTC CTG AAT GAG GCG TGG CTG     706
Pro Asp His Met Thr Leu Trp Arg Gly Phe Leu Asn Glu Ala Trp Leu
     165                 170                 175
ACC GGG ATG CTC CAG CTG TGT CTC TTC GCC ATC ACG GAC CAG GAG AAC     754
Thr Gly Met Leu Gln Leu Cys Leu Phe Ala Thr Thr Asp Gln Glu Asn
180                 185                 190
AAC CCA GCA CTG CCA GGA ACA GAG GCG CTG GTG ATA GGC ATC CTC GTG     802
Asn Pro Ala Leu Pro Gly Thr Glu Ala Leu Val Ile Gly Ile Leu Val
195                 200                 205                 210
GTC ATC ATC GGG GTG TCC CTT GGC ATG AAC ACA GGA TAT GCC ATC AAC     850
Val Ile Ile Gly Val Ser Leu Gly Met Asn Thr Gly Tyr Ala Ile Asn
                215                 220                 225
CCG TCC CGG GAC CTG CCC CCC CGC ATC TTC ACC TTC ATT GCT GGT TGG     898
Pro Ser Arg Asp Leu Pro Pro Arg Ile Phe Thr Phe Ile Ala Gly Trp
          230                 235                 240
GGC AAA CAG GTC TTC AGC AAT GGG GAG AAC TGG TGG TGG GTG CCA GTG     946
Gly Lys Gln Val Phe Ser Asn Gly Glu Asn Trp Trp Trp Val Pro Val
     245                 250                 255
GTG GCA CCA CTT CTG GGT GCC TAT CTA GGT GGC ATC ATC TAC CTG GTC     994
Val Ala Pro Leu Leu Gly Ala Tyr Leu Gly Gly Ile Ile Tyr Leu Val
260                 265                 270
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TTC ATT GGC TCC ACC ATC CCA CGG GAG CCC CTG AAA TTG GAG GAT TCT   1042
Phe Ile Gly Ser Thr Ile Pro Arg Glu Pro Leu Lys Leu Glu Asp Ser
275                 280                 285                 290
GTG GCG TAT GAA GAC CAC GGG ATA ACC GTA TTG CCC AAG ATG GGA TCT   1090
Val Ala Tyr Glu Asp His Gly Ile Thr Val Leu Pro Lys Met Gly Ser
                295                 300                 305
CAT GAA CCC ACG ATC TCT CCC CTC ACC CCC GTC TCT GTG AGC CCT GCC   1138
His Glu Pro Thr Ile Ser Pro Leu Thr Pro Val Ser Val Ser Pro Ala
            310                 315                 320
AAC AGA TCT TCA GTC CAC CCT GCC CCA CCC TTA CAT GAA TCC ATG GCC   1186
Asn Arg Ser Ser Val His Pro Ala Pro Pro Leu His Glu Ser Met Ala
        325                 330                 335
CTA GAG CAC TTC TAAGCAGAGA TTATTTGTGA TCCCATCCAT TCCCCAATAA       1238
Leu Glu His Phe
    340
AGCAAGGCTT GTCCGACAAA                                            1258
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